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Sim

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).

You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

alignment of SEQ ID NO:4 and 17

Sequence 1: UserSeq4, (654 residues)

Sequence 2: UserSeq17, (1246 residues)

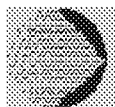
using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

100.0% identity in 654 residues overlap; Score: 3446.0; Gap frequency: 0.0%

```
UserSeq4,      1  QVLKGRMDSEQSPSIGYSSRTLGPNPGLILQALTLSNASDGFNLERLEMLGDSFLKHAIT
UserSeq17,    593 QVLKGRMDSEQSPSIGYSSRTLGPNPGLILQALTLSNASDGFNLERLEMLGDSFLKHAIT
                *****

UserSeq4,      61  TYLFCTYPDAHEGRLSYMRSKKVSNCNLYRLGKKKGLPSRMVVSIFDPPVNWLP PGYVVN
UserSeq17,    653 TYLFCTYPDAHEGRLSYMRSKKVSNCNLYRLGKKKGLPSRMVVSIFDPPVNWLP PGYVVN
                *****

UserSeq4,     121  QDKSNTDKWEKDEMTKDCMLANGKLD EYEEDEEEESLMWRAPKEEADYEDDFLE YDQE
UserSeq17,    713 QDKSNTDKWEKDEMTKDCMLANGKLD EYEEDEEEESLMWRAPKEEADYEDDFLE YDQE
                *****

UserSeq4,     181  HIRFIDNMLMGSGAFVKKISLSPFSTTDSAYEWKMPKKSSLGSM PFSSDFEDFDYSSWDA
UserSeq17,    773 HIRFIDNMLMGSGAFVKKISLSPFSTTDSAYEWKMPKKSSLGSM PFSSDFEDFDYSSWDA
                *****
```

```
UserSeq4,      241 MCYLDPSKAVEEDDFVVGFWNPSEENCGVDTGKQSI SYDLHTEQCIADKSIADCVEALLG
UserSeq17,     833 MCYLDPSKAVEEDDFVVGFWNPSEENCGVDTGKQSI SYDLHTEQCIADKSIADCVEALLG
*****

UserSeq4,      301 CYLTSCGERAAQLFLCSLGLKVL PVIKRTDREKALCPTRENFNSQQKNLSVSCAAASVAS
UserSeq17,     893 CYLTSCGERAAQLFLCSLGLKVL PVIKRTDREKALCPTRENFNSQQKNLSVSCAAASVAS
*****

UserSeq4,      361 SRSSVLKDSEYGCLKIPPRCMFDHPDADKTLNHLISGFENFEKKIN YRFKNKAYLLQAFT
UserSeq17,     953 SRSSVLKDSEYGCLKIPPRCMFDHPDADKTLNHLISGFENFEKKIN YRFKNKAYLLQAFT
*****

UserSeq4,      421 HASYHYNTITDCYQRLEFLGDAILDYLITKHLYEDPRQHSPGVLTD LRSALVNNTIFASL
UserSeq17,    1013 HASYHYNTITDCYQRLEFLGDAILDYLITKHLYEDPRQHSPGVLTD LRSALVNNTIFASL
*****

UserSeq4,      481 AVKYDYHKYFKAVSPELFHVIDDFVQFQLEKNEMQGMSELRRSEED EEEKEEDIEVPKAM
UserSeq17,    1073 AVKYDYHKYFKAVSPELFHVIDDFVQFQLEKNEMQGMSELRRSEED EEEKEEDIEVPKAM
*****

UserSeq4,      541 GDIFESLAGAIYMDSGMSLETVWQVYYPMMRPLIEKFSANVPRSPV RELLEMEPETAKFS
UserSeq17,    1133 GDIFESLAGAIYMDSGMSLETVWQVYYPMMRPLIEKFSANVPRSPV RELLEMEPETAKFS
*****

UserSeq4,      601 PAERTYDGKVRVTVEVVGKGKFKGVGRSYRIAKSAAARRALRSLKAN QPQVPNS
UserSeq17,    1193 PAERTYDGKVRVTVEVVGKGKFKGVGRSYRIAKSAAARRALRSLKAN QPQVPNS
*****
```

39.0% identity in 41 residues overlap; Score: 64.0; Gap frequency: 0.0%

```
UserSeq4,      434 QRLEFLGDAILDYLITKHLYEDPRQHSPGVLTD LRSALVNN
UserSeq17,     637 ERLEMLGDSFLKHAITTYL FCTYPDAHEGRLSYMR SKKVS N
      ***  ***  *   **  *           *  *   **  *  *
```

39.0% identity in 41 residues overlap; Score: 64.0; Gap frequency: 0.0%

```
UserSeq4,      45 ERLEMLGDSFLKHAITTYL FCTYPDAHEGRLSYMR SKKVS N
UserSeq17,    1026 QRLEFLGDAILDYLITKHLYEDPRQHSPGVLTD LRSALVNN
      ***  ***  *   **  *           *  *   **  *  *
```

28.8% identity in 52 residues overlap; Score: 50.0; Gap frequency: 0.0%

```
UserSeq4,      124 SNTDKWEKDEM TKDCMLANGKLDE DYEEDEEEESLMWRAPKEEADYEDDFL
UserSeq17,     797 STTDSAYEWKMPKKSSLGSM PFSSDFEDFDYSSWDAMCYLDPSKAVEEDDFV
      *  **      *  *  *           *  *  *           *           *  ****
```

28.8% identity in 52 residues overlap; Score: 50.0; Gap frequency: 0.0%

```
UserSeq4,      205 STTDSAYEWKMPKKSSLGSM PFSSDFEDFDYSSWDAMCYLDPSKAVEEDDFV
UserSeq17,     716 SNTDKWEKDEM TKDCMLANGKLDE DYEEDEEEESLMWRAPKEEADYEDDFL
```